

1600

RAW SEQUENCE LISTING

DATE: 08/22/2001

PATENT APPLICATION: US/09/835,381

TIME: 10:33:35

Input Set : A:\ES.txt

Output Set: N:\CRF3\08222001\I835381.raw

ENTERED

3 <110> APPLICANT: SUGA, Mikiko
 4 ASAKURA, Yoko
 5 MORI, Yukiko
 6 ITO, Hisao
 7 KURAHASHI, Osamu
 9 <120> TITLE OF INVENTION: ARGININE REPRESSOR DEFICIENT STRAIN OF CORYNEFORM BACTERIUM
 AND METHOD
 10 FOR PRODUCING L-ARGININE
 12 <130> FILE REFERENCE: 206018US0
 14 <140> CURRENT APPLICATION NUMBER: 09/835,381
 15 <141> CURRENT FILING DATE: 2001-04-17
 17 <150> PRIOR APPLICATION NUMBER: JP2000-129167
 18 <151> PRIOR FILING DATE: 2000-04-28
 20 <160> NUMBER OF SEQ ID NOS: 22
 22 <170> SOFTWARE: PatentIn version 3.1
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 25 <211> LENGTH: 32
 26 <212> TYPE: DNA
 27 <213> ORGANISM: Artificial Sequence
 29 <220> FEATURE:
 30 <223> OTHER INFORMATION: synthetic DNA
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 37 <211> LENGTH: 30
 38 <212> TYPE: DNA
 39 <213> ORGANISM: Artificial Sequence
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 49 <211> LENGTH: 26
 50 <212> TYPE: DNA
 51 <213> ORGANISM: Artificial Sequence
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 62 <212> TYPE: DNA
 63 <213> ORGANISM: Artificial Sequence
 65 <220> FEATURE:
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 68 <400> SEQUENCE: 4
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74 <212> TYPE: DNA
75 <213> ORGANISM: Brevibacterium lactofermentum
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79 <222> LOCATION: (1318)..(2598)
80 <223> OTHER INFORMATION:
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88 ctgctgcgct gtgatccaat attcgggggtc gttcactggg tcccctttct gatttctggc      180
90 atagaagaac ccccggtgaac tgtgtggttc cggggggttg tgattttttg gagacttctc      240
92 gcgcaattcc ctagcttagg tgaaaacacc atgaaacact agggaaacac ccatgaaaca      300
94 cccattaggg cagtagggcg gcttcttcgt ctaggggttg catttgggcg gtgatctggg      360
96 ctttagcggtg tgaaagtgtg tcgtaggtgg cgtgctcaat gcactcgaac gtcacgtcat      420
98 ttaccgggtc acggtgggca aagagaacta gtgggttaga cattgttttc ctcgttctcg      480
100 gtggtggtga gcttttctag ccgctcggtg aacgcggcga tcatgaactc ttggagggtt      540
102 tcaccgttct gcatgcctgc gcgcttcctg tcttcacgta gtgccaaagg aacgcgtgcg      600
104 gtgaccacga cgggcttagc ctttgccctgc gcttctagtg cttcgatggg ggcttctgccc      660
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110 caaacattgt cctgcaactc attcattatg tgcagtgttc ctgttactag tcgtacatac      840
112 tcatattttac ctagtctgca tgcagtgcac gcacatgcag tcatgtcgtg ctaatgtgta      900
114 aaacatgtac atgcagattg ctgggggtgc agggggcgga gccaccctgt ccatgcgggg      960
116 tgtgggggctt gccccgccgg tacagacagt gagcaccggg gcacctagtc gcggataccc      1020
118 cccctaggta tcggacacgt aaccctccca tgcgatgca aatctttaac attgagtacg      1080
120 ggtaagctgg cagcctagc caagctaggc ggccaccaa caccactaaa aattaatagt      1140
122 ccctagacaa gacaaacccc cgtgcgagct accaactcat atgcacgggg gccacataac      1200
124 ccgaaggggt ttcaattgac aaccatagca ctagctaaga caacgggcac aacaccgcga      1260
126 caaactcgca ctgcgcaacc ccgcacaaca tcgggtctag gtaacactga aatagaa      1317
128 gtg aac acc tct aag gaa ccg cag gtc aat gag ggt tct aag gtc act      1365
129 Val Asn Thr Ser Lys Glu Pro Gln Val Asn Glu Gly Ser Lys Val Thr
130 1 5 10 15
132 cgc gct agg gcg tgg cgt agg caa aac gtc atg tac aag atc acc aat      1413
133 Arg Ala Arg Ala Trp Arg Arg Gln Asn Val Met Tyr Lys Ile Thr Asn
134 20 25 30
136 agt aag gct ctg gcg ggg tgc cat agg tgg cgc agg gac gaa gct gtt      1461
137 Ser Lys Ala Leu Ala Gly Cys His Arg Trp Arg Arg Asp Glu Ala Val
138 35 40 45
140 gcg gtg tcc tgg tgc tct aac ggt gct tgc cag ttt gag ggt ctg caa      1509
141 Ala Val Ser Trp Ser Ser Asn Gly Ala Ser Gln Phe Glu Gly Leu Gln
142 50 55 60
144 aac tct cac tct cgc tgg ggg tca cct ctg gct gaa ttg gaa gtc atg      1557
145 Asn Ser His Ser Arg Trp Gly Ser Pro Leu Ala Glu Leu Glu Val Met
146 65 70 75 80
148 ggc gaa cgc cgc att gag ctg gct att gct act aag aat cac ttg gcg      1605
149 Gly Glu Arg Arg Ile Glu Leu Ala Ile Ala Thr Lys Asn His Leu Ala
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154				100					105					110			
156	tca	cag	tca	ttt	gcg	cag	gtt	gaa	gcg	ggt	att	aag	act	gcg	tac	tct	1701
157	Ser	Gln	Ser	Phe	Ala	Gln	Val	Glu	Ala	Gly	Ile	Lys	Thr	Ala	Tyr	Ser	
158				115					120					125			
160	tcg	atg	gtg	aaa	aca	tct	cag	tgg	aag	aaa	gaa	cgt	gca	cgg	tac	ggg	1749
161	Ser	Met	Val	Lys	Thr	Ser	Gln	Trp	Lys	Lys	Glu	Arg	Ala	Arg	Tyr	Gly	
162				130					135					140			
164	gtg	gag	cac	acc	tat	agt	gac	tat	gag	gtc	aca	gac	tct	tgg	gcg	aac	1797
165	Val	Glu	His	Thr	Tyr	Ser	Asp	Tyr	Glu	Val	Thr	Asp	Ser	Trp	Ala	Asn	
166	145						150				155					160	
168	ggt	tgg	cac	ttg	cac	cgc	aac	atg	ctg	ttg	ttc	ttg	gat	cgt	cca	ctg	1845
169	Gly	Trp	His	Leu	His	Arg	Asn	Met	Leu	Leu	Phe	Leu	Asp	Arg	Pro	Leu	
170				165					170					175			
172	tct	gac	gat	gaa	ctc	aag	gcg	ttt	gag	gat	tcc	atg	ttt	tcc	cgc	tgg	1893
173	Ser	Asp	Asp	Glu	Leu	Lys	Ala	Phe	Glu	Asp	Ser	Met	Phe	Ser	Arg	Trp	
174				180					185					190			
176	tct	gct	ggt	gtg	gtt	aag	gcc	ggt	atg	gac	gcg	cca	ctg	cgt	gag	cac	1941
177	Ser	Ala	Gly	Val	Val	Lys	Ala	Gly	Met	Asp	Ala	Pro	Leu	Arg	Glu	His	
178				195					200					205			
180	ggg	gtc	aaa	ctt	gat	cag	gtg	tct	acc	tgg	ggt	gga	gac	gct	gcg	aaa	1989
181	Gly	Val	Lys	Leu	Asp	Gln	Val	Ser	Thr	Trp	Gly	Gly	Asp	Ala	Ala	Lys	
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184	atg	gca	acc	tac	ctc	gct	aag	ggc	atg	tct	cag	gaa	ctg	act	ggc	tcc	2037
185	Met	Ala	Thr	Tyr	Leu	Ala	Lys	Gly	Met	Ser	Gln	Glu	Leu	Thr	Gly	Ser	
186	225						230				235					240	
188	gct	act	aaa	acc	gcg	tct	aag	ggg	tcg	tac	acg	ccg	ttt	cag	atg	ttg	2085
189	Ala	Thr	Lys	Thr	Ala	Ser	Lys	Gly	Ser	Tyr	Thr	Pro	Phe	Gln	Met	Leu	
190				245					250					255			
192	gat	atg	ttg	gcc	gat	caa	agc	gac	gcc	ggc	gag	gat	atg	gac	gct	gtt	2133
193	Asp	Met	Leu	Ala	Asp	Gln	Ser	Asp	Ala	Gly	Glu	Asp	Met	Asp	Ala	Val	
194				260					265					270			
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204	gac	gct	gat	gta	cgt	cgt	gaa	atg	gaa	gaa	gaa	ctg	tac	aag	ctc	gcc	2277
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212	ttg	gtg	aag	ccc	gat	gat	tgg	aaa	ctg	att	cag	tct	gat	ttc	gcg	gtt	2373
213	Leu	Val	Lys	Pro	Asp	Asp	Trp	Lys	Leu	Ile	Gln	Ser	Asp	Phe	Ala	Val	
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216	agg	cag	tac	gtt	cta	gat	tgc	gtg	gat	aag	gct	aag	gac	gtg	gcc	gct	2421
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224 acc ccg tgc atg atc gtt atg gat gat gtg gac ttg gac gcg gtt ctg      2517
225 Thr Pro Cys Met Ile Val Met Asp Asp Val Asp Leu Asp Ala Val Leu
226 385          390          395          400
228 cct act cat ggg gac gct act aag cgt gat ctg aat gcg gcg gtg ttc      2565
229 Pro Thr His Gly Asp Ala Thr Lys Arg Asp Leu Asn Ala Ala Val Phe
230          405          410          415
232 gcg ggt aat gag cag act att ctt cgc acc cac taaaagcggc ataaaccccg      2618
233 Ala Gly Asn Glu Gln Thr Ile Leu Arg Thr His
234          420          425
236 ttcgatattt tgtgcgatga atttatggtc aatgtgcggg gggcaaaacta tgatgggtct      2678
238 tgttgttgac aatggctgat ttcatacagga atggaactgt catgctgtta tgtgcctggc      2738
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244 gcacaccata gtgggcatga gtaataccta cgcgcgcgtg ggctagggct taacgcgcgt      2918
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315 35 40 45
318 Ala Val Ser Trp Ser Ser Asn Gly Ala Ser Gln Phe Glu Gly Leu Gln
319 50 55 60
322 Asn Ser His Ser Arg Trp Gly Ser Pro Leu Ala Glu Leu Glu Val Met
323 65 70 75 80
326 Gly Glu Arg Arg Ile Glu Leu Ala Ile Ala Thr Lys Asn His Leu Ala
327 85 90 95
330 Ala Gly Gly Ala Leu Met Met Phe Val Gly Thr Val Arg His Asn Arg
331 100 105 110
334 Ser Gln Ser Phe Ala Gln Val Glu Ala Gly Ile Lys Thr Ala Tyr Ser
335 115 120 125
338 Ser Met Val Lys Thr Ser Gln Trp Lys Lys Glu Arg Ala Arg Tyr Gly
339 130 135 140
342 Val Glu His Thr Tyr Ser Asp Tyr Glu Val Thr Asp Ser Trp Ala Asn
343 145 150 155 160
346 Gly Trp His Leu His Arg Asn Met Leu Leu Phe Leu Asp Arg Pro Leu
347 165 170 175
350 Ser Asp Asp Glu Leu Lys Ala Phe Glu Asp Ser Met Phe Ser Arg Trp
351 180 185 190
354 Ser Ala Gly Val Val Lys Ala Gly Met Asp Ala Pro Leu Arg Glu His
355 195 200 205
358 Gly Val Lys Leu Asp Gln Val Ser Thr Trp Gly Gly Asp Ala Ala Lys
359 210 215 220
362 Met Ala Thr Tyr Leu Ala Lys Gly Met Ser Gln Glu Leu Thr Gly Ser
363 225 230 235 240
366 Ala Thr Lys Thr Ala Ser Lys Gly Ser Tyr Thr Pro Phe Gln Met Leu
367 245 250 255
370 Asp Met Leu Ala Asp Gln Ser Asp Ala Gly Glu Asp Met Asp Ala Val
371 260 265 270
374 Leu Val Ala Arg Trp Arg Glu Tyr Glu Val Gly Ser Lys Asn Leu Arg
375 275 280 285
378 Ser Ser Trp Ser Arg Gly Ala Lys Arg Ala Leu Gly Ile Asp Tyr Ile
379 290 295 300
382 Asp Ala Asp Val Arg Arg Glu Met Glu Glu Glu Leu Tyr Lys Leu Ala
383 305 310 315 320
386 Gly Leu Glu Ala Pro Glu Arg Val Glu Ser Thr Arg Val Ala Val Ala
387 325 330 335
390 Leu Val Lys Pro Asp Asp Trp Lys Leu Ile Gln Ser Asp Phe Ala Val
391 340 345 350
394 Arg Gln Tyr Val Leu Asp Cys Val Asp Lys Ala Lys Asp Val Ala Ala
395 355 360 365
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